WEST Search History

Hide Items Restore Clear Cancel

DATE: Wednesday, May 17, 2006

Hide?	Set Name	Query	Hit Count
		DB=EPAB; THES=ASSIGNEE; PLUR=YES; OP=ADJ	
☐	L6	WO-2005114173-A2.did.	0
		DB=USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ	
☐	L5	(human double minute 2 protein or hdm2 or mdm2) same solid support	6
		DB=PGPB; THES=ASSIGNEE; PLUR=YES; OP=ADJ	
☐	L4	(human double minute 2 protein or hdm2 or mdm2) same solid support	10
☐	L3	(human double minute 2 protein or hdm2 or mdm2) same crystal	20
		DB=USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ	
☐	L2	(human double minute 2 protein or hdm2 or mdm2) same crystal	9
☐	L1	human double minute 2 protein or hdm2 or mdm2	471

END OF SEARCH HISTORY

```
FILE 'HOME' ENTERED AT 17:23:40 ON 17 MAY 2006

=> file .nash
=> s (human double minute 2 protein or HDM2 or MDM2) and crystal and x-ray
L1            7 FILE MEDLINE
L2            9 FILE CAPLUS
L3            4 FILE SCISEARCH
L4            0 FILE LIFESCI
L5            1 FILE BIOSIS
L6            5 FILE EMBASE

TOTAL FOR ALL FILES
L7           26 (HUMAN DOUBLE MINUTE 2 PROTEIN OR HDM2 OR MDM2) AND CRYSTAL AND
                X-RAY

=> s l7 not 2003-2006/py
L14           3 L7 NOT 2003-2006/PY

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15           3 DUP REM L14 (0 DUPLICATES REMOVED)

=> d ibib abs 1-3

L15  ANSWER 1 OF 3     MEDLINE on STN
ACCESSION NUMBER:    2001552034     MEDLINE Full-text
DOCUMENT NUMBER:     PubMed ID: 11599019
TITLE:               QSAR: hydropathic analysis of inhibitors of the p53-
                     mdm2 interaction.
AUTHOR:              Galatin P S; Abraham D J
CORPORATE SOURCE:    Department of Medicinal Chemistry and Institute for
                     Structural Biology and Drug Discovery, Virginia
                     Commonwealth University, Richmond, Virginia 23298, USA.
SOURCE:              Proteins, (2001 Nov 15) Vol. 45, No. 3, pp. 169-75.
                     Journal code: 8700181. ISSN: 0887-3585.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200112
ENTRY DATE:          Entered STN: 15 Oct 2001
                     Last Updated on STN: 22 Jan 2002
                     Entered Medline: 17 Dec 2001
AB      To date, a number of p53-derived peptides have been evaluated in vitro for their ability
        to inhibit the carcinogenic p53-mdm2 interaction. Design of second-generation nonpeptidic
        compounds requires the reduction of large peptide structures down to small molecules
        maintaining the proper spatial arrangement of key functional groups.  Molecular modeling
        software exists that can predict and rank intermolecular interactions from the p53- mdm2
        complex crystal structure.  Such analyses can yield a pharmacophore model suitable as a
        search query for a 3D chemical database to generate new lead compounds.  As preliminary
        validation of this methodology, the Hydropathic INTeractions (HINT) program has been used
        to generate noncovalent interaction measurements between reported peptide inhibitors and
        mdm2.  Quantitative structure-activity relationships were developed expressing peptide
        activity as a linear combination of hydropathic descriptors.  In general, HINT
        measurements accurately modeled the effects of even single-atom alterations of the p53-
        peptide structure on activity, accounting for 70-90% of variation in experimental
        inhibition constants.  These results surpassed those of a recently described molecular
        dynamics-based approach and required significantly less computation time.  In conclusion,
        the HINT program can be integrated into the drug design cycle for next-generation p53-
        mdm2 complex inhibitors with confidence in its ability to simulate this noteworthy
        protein-protein interaction. Copyright 2001 Wiley-Liss, Inc.


L15  ANSWER 2 OF 3  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2000:786354  CAPLUS Full-text
DOCUMENT NUMBER:          134:82478
TITLE:                    Study on the structure of inhibitors of the
                          MDM2 oncogene
AUTHOR(S):                An, Dong-ge; Tu, Guang-zhong; Yin, Da-li; He, Wen-yi;
                          Ma, Li-bin; Kong, Man
```

```
CORPORATE SOURCE:        Inst. Materia Med., Chinese Acad. Med. Sci., Beijing,
                         100050, Peop. Rep. China
SOURCE:                  Bopuxue Zazhi (2000), 17(5), 383-388
                         CODEN: BOZAE2; ISSN: 1000-4556
PUBLISHER:               Zhongguo Kexueyuan Wuhan Wuli Yanjiuso
DOCUMENT TYPE:           Journal
LANGUAGE:                Chinese
AB       The MDM2 oncoprotein is a cellular inhibitor of the P53 tumor suppressor in that it can
         bind the transactivation domain of P53 and down-regulate its ability to activate
         transcription.  In certain cancers, MDM2 amplification is a common event and contributes
         to the inactivation of P53.  The crystal structure of the MDM2 bound to P53 has been
         analyzed through x-ray crystallog.  The crystal structure provides a framework for the
         discovery of compds. that may prevent the activation of the P53 tumor suppressor by the
         MDM2 oncogene in cancer.  Inhibitors of the MDM2 oncogene have been synthesized on the
         base of this theory. All assignments of inhibitors were obtained from 1H, 13C, 1H-1H COSY,
         HMQC and HMBC spectra.  With regard to count space distance of two benzene rings, three-
         bond coupling consts. were utilized to determine the structure of inhibitors.
         Stereostructures and relative configurations were discussed, and dominant energy was
         computed by using Sybyl software.


L15  ANSWER 3 OF 3      MEDLINE on STN
ACCESSION NUMBER:    97081050     MEDLINE Full-text
DOCUMENT NUMBER:     PubMed ID: 8875929
TITLE:               Structure of the MDM2 oncoprotein bound to the
                     p53 tumor suppressor transactivation domain.
AUTHOR:              Kussie P H; Gorina S; Marechal V; Elenbaas B; Moreau J;
                     Levine A J; Pavletich N P
CORPORATE SOURCE:    Cellular Biochemistry and Biophysics Program, Memorial
                     Sloan-Kettering Cancer Center, New York, NY 10021, USA..
                     nikola@xray2.mskcc.org
CONTRACT NUMBER:     CA65698 (NCI)
SOURCE:              Science, (1996 Nov 8) Vol. 274, No. 5289, pp. 948-53.
                     Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Commentary
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
OTHER SOURCE:        PDB-1YCQ; PDB-1YCR
ENTRY MONTH:         199612
ENTRY DATE:          Entered STN: 28 Jan 1997
                     Last Updated on STN: 28 Jan 1997
                     Entered Medline: 6 Dec 1996
AB       The MDM2 oncoprotein is a cellular inhibitor of the p53 tumor suppressor in that it can
         bind the transactivation domain of p53 and downregulate its ability to activate
         transcription.  In certain cancers, MDM2 amplification is a common event and contributes
         to the inactivation of p53.  The crystal structure of the 109-residue amino-terminal
         domain of MDM2 bound to a 15-residue transactivation domain peptide of p53 revealed that
         MDM2 has a deep hydrophobic cleft on which the p53 peptide binds as an amphipathic alpha
         helix.  The interface relies on the steric complementarity between the MDM2 cleft and the
         hydrophobic face of the p53 alpha helix and, in particular, on a triad of p53 amino acids-
         Phe19, Trp23, and Leu26-which insert deep into the MDM2 cleft.  These same p53 residues
         are also involved in transactivation, supporting the hypothesis that MDM2 inactivates p53
         by concealing its transactivation domain.  The structure also suggests that the
         amphipathic alpha helix may be a common structural motif in the binding of a diverse
         family of transactivation factors to the TATA-binding protein-associated factors.

=> s (human double minute 2 protein or HDM2 or MDM2) and crystal
TOTAL FOR ALL FILES
L22         119 (HUMAN DOUBLE MINUTE 2 PROTEIN OR HDM2 OR MDM2) AND CRYSTAL

=> s l22 not 2003-2006/py

TOTAL FOR ALL FILES
L29          41 L22 NOT 2003-2006/PY

=> dup rem l29
PROCESSING COMPLETED FOR L29
L30          22 DUP REM L29 (19 DUPLICATES REMOVED)
```

```
=> d ibib abs 1-22

L30  ANSWER 1 OF 22  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:     2003:132808  SCISEARCH Full-text
THE GENUINE ARTICLE: 639NT
TITLE:                Cell cycle regulatory E3 ubiquitin ligases as anticancer
                      targets
AUTHOR:               Pray T R; Parlati F; Huang J N; Wong B R; Payan D G;
                      Bennett M K; Issakani S D; Molineaux S; Demo S D (Reprint)
CORPORATE SOURCE:     Rigel Pharmaceut Inc, 240 E Grand Ave, San Francisco, CA
                      94080 USA (Reprint); Rigel Pharmaceut Inc, San Francisco,
                      CA 94080 USA
COUNTRY OF AUTHOR:    USA
SOURCE:               DRUG RESISTANCE UPDATES, (DEC 2002) Vol. 5, No. 6, pp.
                      249-258.
                      ISSN: 1368-7646.
PUBLISHER:            CHURCHILL LIVINGSTONE, JOURNAL PRODUCTION DEPT, ROBERT
                      STEVENSON HOUSE, 1-3 BAXTERS PLACE, LEITH WALK, EDINBURGH
                      EH1 3AF, MIDLOTHIAN, SCOTLAND.
DOCUMENT TYPE:        General Review; Journal
LANGUAGE:             English
REFERENCE COUNT:      81
ENTRY DATE:           Entered STN: 21 Feb 2003
                      Last Updated on STN: 21 Feb 2003
                     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB         Disregulation of the cell cycle and proliferation play key roles in cellular
           transformation and tumorigenesis.  Such processes are intimately tied to the
           concentration, localization and activity of enzymes, adapters, receptors, and
           structural proteins in cells.  Ubiquitination of these cellular regulatory
           proteins, governed by specific enzymes in the ubiquitin (Ub) conjugation cascade,
           has profound effects on their various functions, most commonly through proteasome
           targeting and degradation. This review will focus on a variety of E3 Ub ligases as
           potential oncology drug targets, with particular emphasis on the role of these
           molecules in the regulation of stability, localization, and activity of key
           proteins such as tumor suppressors and oncoproteins.  E3 ubiquitin ligases that
           have established roles in cell cycle and apoptosis, such as the anaphase-promoting
           complex (APC), the Skp-1-Cull-F-box class, and the murine double minute 2 (MDM2)
           protein, in addition to more recently discovered E3 ubiquitin ligases which may be
           similarly important in tumorigenesis, (e.g.  Smurf family, CHFR, and Efp), will be
           discussed. We will present evidence to support E3 ligases as good biological
           targets in the development of anticancer therapeutics and address challenges in
           drug discovery for these targets. (C) 2002 Elsevier Science Ltd.  All rights
           reserved.


L30  ANSWER 2 OF 22  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:     2001:949055  SCISEARCH Full-text
THE GENUINE ARTICLE: 494ZM
TITLE:                Identification of p53 sequence elements that are required
                      for MDM2-mediated nuclear export
AUTHOR:               Gu J J; Nie L H; Wiederschain D; Yuan Z M (Reprint)
CORPORATE SOURCE:     Harvard Univ, Sch Publ Hlth, Dept Canc Cell Biol, Bldg 1,
                      Room 209, 665 Huntington Ave, Boston, MA 02115 USA
                      (Reprint); Harvard Univ, Sch Publ Hlth, Dept Canc Cell
                      Biol, Boston, MA 02115 USA
COUNTRY OF AUTHOR:    USA
SOURCE:               MOLECULAR AND CELLULAR BIOLOGY, (DEC 2001) Vol. 21, No.
                      24, pp. 8533-8546.
                      ISSN: 0270-7306.
PUBLISHER:            AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC
                      20036-2904 USA.
DOCUMENT TYPE:        Article; Journal
LANGUAGE:             English
REFERENCE COUNT:      22
ENTRY DATE:           Entered STN: 7 Dec 2001
                      Last Updated on STN: 7 Dec 2001
                     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB         It has been demonstrated that MDM2 can differentially regulate subcellular
           distribution of p53 and its close structural homologue p73.  In contrast to MDM2-
```

mediated p53 nuclear export, p73 accumulates in the nucleus as aggregates that colocalize with MDM2. Distinct distribution patterns of p53 and p73 suggest the existence of unique structural elements in the two homologues that determine their MDM2-mediated relocalization in the cell. Using a series of p53/p73 chimeric proteins, we demonstrate that three regions of p53 are:involved in the regulation of MDM2-mediated nuclear export. The DNA binding domain (DBD) is involved in the maintenance of a proper conformation that is required for functional activity of the nuclear export sequence (NES) of p53. The extreme C terminus of p53 harbors several lysine residues whose ubiquitination by MDM2 appears to be the initial event in p53 nuclear export, as evidenced by the impaired nucleocytoplasmic shuttling of p53 mutants bearing simultaneous substitutions of lysines 370, 372, 373, 381, 382, and 386 to arginines (6KR) or alanines (6KA). Finally, the region between the DBD and the oligomerization domain of p53, specifically lysine 305, also plays a critical role in fully revealing p53NES. We conclude that MDM2 - mediated nuclear export of p53 depends on a series of ubiquitination-induced conformational changes in the p53 molecule that lead to the activation of p53NES. In addition, we demonstrate that the p53NES may be activated without necessarily disrupting the p53 tetramer.

```
L30  ANSWER 3 OF 22      MEDLINE on STN              DUPLICATE 1
ACCESSION NUMBER:    2002073387     MEDLINE Full-text
DOCUMENT NUMBER:     PubMed ID: 11800560
TITLE:               Virtual interaction profiles of proteins.
AUTHOR:              Wollacott A M; Desjarlais J R
CORPORATE SOURCE:    Department of Chemistry, Pennsylvania State University, 406
                     Chandlee Laboratory, PA 16802, USA.
SOURCE:              Journal of molecular biology, (2001 Oct 19) Vol. 313, No.
                     2, pp. 317-42.
                     Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY:        England: United Kingdom
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200202
ENTRY DATE:          Entered STN: 25 Jan 2002
                     Last Updated on STN: 5 Feb 2002
                     Entered Medline: 4 Feb 2002
```

AB We have developed a new method for the prediction of peptide sequences that bind to a protein, given a three-dimensional structure of the protein in complex with a peptide. By applying a recently developed sequence prediction algorithm and a novel ensemble averaging calculation, we generate a diverse collection of peptide sequences that are predicted to have significant affinity for the protein. Using output from the simulations, we create position-specific scoring matrices, or virtual interaction profiles (VIPs). Comparison of VIPs for a collection of binding motifs to sequences determined experimentally indicates that the prediction algorithm is accurate and applicable to a diverse range of structures. With these VIPs, one can scan protein sequence databases rapidly to seek binding partners of potential biological significance. Overall, this method can significantly enhance the information contained within a protein- peptide crystal structure, and enrich the data obtained by experimental selection methods such as phage display. Copyright 2001 Academic Press.

```
L30  ANSWER 4 OF 22      MEDLINE on STN              DUPLICATE 2
ACCESSION NUMBER:    2001552034     MEDLINE Full-text
DOCUMENT NUMBER:     PubMed ID: 11599019
TITLE:               QSAR: hydropathic analysis of inhibitors of the p53-
                     mdm2 interaction.
AUTHOR:              Galatin P S; Abraham D J
CORPORATE SOURCE:    Department of Medicinal Chemistry and Institute for
                     Structural Biology and Drug Discovery, Virginia
                     Commonwealth University, Richmond, Virginia 23298, USA.
SOURCE:              Proteins, (2001 Nov 15) Vol. 45, No. 3, pp. 169-75.
                     Journal code: 8700181. ISSN: 0887-3585.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200112
ENTRY DATE:          Entered STN: 15 Oct 2001
                     Last Updated on STN: 22 Jan 2002
```

Entered Medline: 17 Dec 2001

AB To date, a number of p53-derived peptides have been evaluated in vitro for their ability to inhibit the carcinogenic p53-**mdm2** interaction. Design of second-generation nonpeptidic compounds requires the reduction of large peptide structures down to small molecules maintaining the proper spatial arrangement of key functional groups. Molecular modeling software exists that can predict and rank intermolecular interactions from the p53- **mdm2** complex crystal structure. Such analyses can yield a pharmacophore model suitable as a search query for a 3D chemical database to generate new lead compounds. As preliminary validation of this methodology, the Hydropathic INTeractions (HINT) program has been used to generate noncovalent interaction measurements between reported peptide inhibitors and **mdm2**. Quantitative structure-activity relationships were developed expressing peptide activity as a linear combination of hydropathic descriptors. In general, HINT measurements accurately modeled the effects of even single-atom alterations of the p53-peptide structure on activity, accounting for 70-90% of variation in experimental inhibition constants. These results surpassed those of a recently described molecular dynamics-based approach and required significantly less computation time. In conclusion, the HINT program can be integrated into the drug design cycle for next-generation p53-**mdm2** complex inhibitors with confidence in its ability to simulate this noteworthy protein-protein interaction. Copyright 2001 Wiley-Liss, Inc.

L30 ANSWER 5 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:103794 SCISEARCH Full-text
THE GENUINE ARTICLE: 635KA
TITLE: Rescuing the function of mutant p53
AUTHOR: Bullock A N; Fersht A (Reprint)
CORPORATE SOURCE: Univ Cambridge, Chem Lab, Lensfield Rd, Cambridge CB2 1EW, England (Reprint); Univ Cambridge, Chem Lab, Cambridge CB2 1EW, England; Univ Cambridge, MRC, Ctr Prot Engn, Cambridge CB2 1EW, England
arf10@cam.ac.uk
COUNTRY OF AUTHOR: England
SOURCE: NATURE REVIEWS CANCER, (OCT 2001) Vol. 1, No. 1, pp. 68-76
ISSN: 1474-175X.
PUBLISHER: NATURE PUBLISHING GROUP, MACMILLAN BUILDING, 4 CRINAN ST, LONDON N1 9XW, ENGLAND.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 71
ENTRY DATE: Entered STN: 7 Feb 2003
Last Updated on STN: 20 Oct 2005

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB One protein - p53 - plays nemesis to most cancers by condemning damaged cells to death or quarantining them for repair. But the activity of p53 relies on its intact native conformation, which can be lost following mutation of a single nucleotide. With thousands of such mutations identified in patients, how can a future cancer drug buttress this fragile protein structure and restore the cell's natural defence?.

L30 ANSWER 6 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2000:282555 SCISEARCH Full-text
THE GENUINE ARTICLE: 301DG
TITLE: Tumor-derived mutations within the DNA-binding domain of p53 that phenotypically resemble the deletion of the proline-rich domain
AUTHOR: Roth J; Koch P; Contente A; Dobbelstein M (Reprint)
CORPORATE SOURCE: Univ Marburg, Inst Virol, Zentrum Mikrobiol & Hyge, Robert Koch Str 17, D-35037 Marburg, Germany (Reprint); Univ Marburg, Inst Virol, Zentrum Mikrobiol & Hyge, D-35037 Marburg, Germany; Univ Marburg, Zentrum Innere Med, Abt Gastroenterol & Stoffwechsel, Fachbereich Med, D-35043 Marburg, Germany
COUNTRY OF AUTHOR: Germany
SOURCE: ONCOGENE, (30 MAR 2000) Vol. 19, No. 14, pp. 1834-1842.
ISSN: 0950-9232.
PUBLISHER: NATURE PUBLISHING GROUP, HOUNDMILLS, BASINGSTOKE RG21 6XS, HAMPSHIRE, ENGLAND.

DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 45
ENTRY DATE: Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The p53 tumor suppressor protein induces apoptosis through a mechanism that may involve the transcriptional activation of cellular genes, including the PIG3 gene. A p53 protein lacking the proline-rich region (p53 Delta 62-91) induces many p53-responsive genes but not PIG3, In parallel, this mutant induces growth arrest but not apoptosis, We show here that the replacement of the N-terminal (amino acids 1-80) or C-terminal (amino acids 344-393) domains of p53 with heterologous domains does not interfere with transcription from the PIG3 promoter, but these chimeras still require the proline-rich region for PIG3 activation. The p53-homolog p73 beta also activated the PIG3 promoter, but in contrast to p53, the proline-rich domain of p73 beta (residues 81-113) was dispensable to induce the PIG3 promoter, Some tumor-derived p53-mutants, especially M246I, retained the ability to activate transcription of mdm2 but specifically failed to induce the PIG3 promoter, thus resembling p53 Delta 62-91. Further, p53 Delta 62-91 and p53M246I were defective for induction of apoptosis, Finally, p53 Delta 62-91 and p53M246I both showed reduced binding to the DNA of the PIG3 promoter and also to the DNA of the mdm2 and p21 promoters in vitro. Correspondingly, at low expression levels, p53 Delta 62-91 and p53M246I poorly activated the mdm2 promoter when compared to wild type p53. Our results suggest that the proline-rich domain of p53 affects the ability of the central domain to bind DNA, Moreover, some tumor-derived mutations within the central DNA binding domain of p53 mimic the loss of the proline-rich domain.

L30 ANSWER 7 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:561574 SCISEARCH Full-text
THE GENUINE ARTICLE: 335CC
TITLE: The C-terminal regulatory domain of p53 contains a functional docking site for cyclin A
AUTHOR: Luciani M G; Hutchins J R A; Zheleva D; Hupp T R (Reprint)
CORPORATE SOURCE: Univ Dundee, Sch Med, Dept Mol & Cellular Pathol, Dundee DD1 9SY, Scotland (Reprint); Univ Dundee, Sch Med, Canc Res Campaign Labs, Dundee DD1 9SY, Scotland; Univ Dundee, Sch Med, Biomed Res Ctr, Dundee DD1 9SY, Scotland; Cyclacel Ltd, Dundee DD1 5JJ, Scotland
COUNTRY OF AUTHOR: Scotland
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (14 JUL 2000) Vol. 300, No. 3, pp. 503-518.
ISSN: 0022-2836.
PUBLISHER: ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON NW1 7DX, ENGLAND

DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 54
ENTRY DATE: Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Radiation injury to cells enhances C-terminal phosphorylation of p53 at both Ser315 and Ser392 in vivo, suggesting the existence of two cooperating DNA damage-responsive pathways that play a role in stimulating p53-dependent gene expression. Our previous data has shown that cyclin A-cdk2 is the major enzyme responsible for modifying p53 at Ser315 in vivo after irradiation damage and in this report we dissect the mechanism of cyclinA-cdk2 binding to and phosphorylation of p53. Although cyclin B-1-dependent protein kinases can phosphorylate small peptides containing the Ser315 site, cyclin A-cdk2 does not phosphorylate such small peptides suggesting that additional determinants are required for cyclin A-cdk2 interaction with p53 Peptide competition studies have localized a cyclin A interaction site to a Lys381Lys382Leu383Met384Phe385 sequence within C-terminaI negative regulatory domain of human p53. An alanine mutation at any one of four key positions abrogates the efficacy of a synthetic peptide containing this motif as an inhibitor of cyclin A-cdk2 phosphorylation of F53 protein. Single amino acid mutations of full-length p53 protein at Lys382, Leu383, or Phe385 decreases cyclin A-cdk2 dependent phosphorylation at Ser315. Cyclin B-1-cdk2 complexes are not inhibited by KKLMF motif-containing peptides nor is p53 phosphorylation by cyclin B-cdk2 reduced by mutation of the cyclin A interaction site. These data identifying a KKLMF cyclin A docking site on p53 protein highlight a common cyclin

```
             A interaction motif that is shared between the tumour suppressor proteins pRb and
             p53. (C) 2000 Academic Press.


L30  ANSWER 8 OF 22  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2000:786354  CAPLUS Full-text
DOCUMENT NUMBER:          134:82478
TITLE:                    Study on the structure of inhibitors of the
                          MDM2 oncogene
AUTHOR(S):                An, Dong-ge; Tu, Guang-zhong; Yin, Da-li; He, Wen-yi;
                          Ma, Li-bin; Kong, Man
CORPORATE SOURCE:         Inst. Materia Med., Chinese Acad. Med. Sci., Beijing,
                          100050, Peop. Rep. China
SOURCE:                   Bopuxue Zazhi (2000), 17(5), 383-388
                          CODEN: BOZAE2; ISSN: 1000-4556
PUBLISHER:                Zhongguo Kexueyuan Wuhan Wuli Yanjiuso
DOCUMENT TYPE:            Journal
LANGUAGE:                 Chinese
AB     The MDM2 oncoprotein is a cellular inhibitor of the P53 tumor suppressor in that it can
       bind the transactivation domain of P53 and down-regulate its ability to activate
       transcription.  In certain cancers, MDM2 amplification is a common event and contributes
       to the inactivation of P53.  The crystal structure of the MDM2 bound to P53 has been
       analyzed through x-ray crystallog.  The crystal structure provides a framework for the
       discovery of compds. that may prevent the activation of the P53 tumor suppressor by the
       MDM2 oncogene in cancer.  Inhibitors of the MDM2 oncogene have been synthesized on the
       base of this theory.  All assignments of inhibitors were obtained from 1H, 13C, 1H-1H
       COSY, HMQC and HMBC spectra.  With regard to count space distance of two benzene rings,
       three-bond coupling consts. were utilized to determine the structure of inhibitors.
       Stereostructures and relative configurations were discussed, and dominant energy was
       computed by using Sybyl software.


L30  ANSWER 9 OF 22  CAPLUS  COPYRIGHT 2006 ACS on STN DUPLICATE 3
ACCESSION NUMBER:         2000:269098  CAPLUS Full-text
DOCUMENT NUMBER:          133:53086
TITLE:                    Combined molecular mechanical and continuum solvent
                          approach (MM-PBSA/GBSA) to predict ligand binding
AUTHOR(S):                Massova, Irina; Kollman, Peter A.
CORPORATE SOURCE:         Department of Pharmaceutical Chemistry, University of
                          California at San Francisco, San Francisco, CA,
                          94143-0446, USA
SOURCE:                   Perspectives in Drug Discovery and Design (2000),
                          18(Hydrophobicity and Solvation in Drug Design, Pt.
                          II), 113-135
                          CODEN: PDDDEC; ISSN: 0928-2866
PUBLISHER:                Kluwer Academic Publishers
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB     Significant progress has been achieved in computational methods to treat solvent effects
       in recent years.  Among various techniques, the continuum solvent approach appears to be
       practically promising because it can be used to calculate reliable interaction and
       solvation energies in complex systems.  A computational scanning mutagenesis method, one
       of such new approaches, has been recently developed.  It combines the mol. mech. and
       continuum solvent approaches and allows one to identify the "hot spots" in binding
       interfaces from a single trajectory of a wild type complex.  Such techniques can be also
       used as a tool to optimize the interacting species for the binding, or as a ranking
       procedure in high throughput screening.
REFERENCE COUNT:          57     THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS
                                 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30  ANSWER 10 OF 22  EMBASE  COPYRIGHT (c) 2006 Elsevier B.V. All rights
     reserved on STN
ACCESSION NUMBER:    1999329540  EMBASE  Full-text
TITLE:               Computational alanine scanning to probe protein-protein
                     interactions: A novel approach to evaluate binding free
                     energies.
AUTHOR:              Massova I.; Kollman P.A.
CORPORATE SOURCE:    P.A. Kollman, Dept. of Pharmaceutical Chemistry, University
                     of California, San Francisco, CA 94143-0446, United States.
                     pak@cgl.ucsf.edu
SOURCE:              Journal of the American Chemical Society, (15 Sep 1999)
```

Vol. 121, No. 36, pp. 8133-8143. .
ISSN: 0002-7863 CODEN: JACSAT
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 7 Oct 1999
Last Updated on STN: 7 Oct 1999

AB Noncovalent interactions are important in many physiological processes of complexation which involve all components of the living cells. Here we report an approach to computationally study the interaction free energies in protein-protein complexes which allows from a single simulation an estimate of the individual contribution of each residue to the binding. We developed this new technique - computational alanine scanning - and applied it to study the interactions of the oncoprotein Mdm2 to the N-terminal stretch of tumor suppressor protein p53. Excellent agreement has been found between the calculated and experimental data. This residue mutation methodology could prove to be a useful general design tool for molecules - nucleotides, peptides, lipids, or any other organic compound - optimized for interactions or stability, since one can qualitatively estimate the free energy consequences of many mutations from a single molecular dynamics trajectory.

L30 ANSWER 11 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1999:825800 SCISEARCH Full-text
THE GENUINE ARTICLE: 249XU
TITLE: The stabilization mechanism of mutant-type p53 by impaired ubiquitination: the loss of wild-type p53 function and the hsp90 association
AUTHOR: Nagata Y; Anan T; Yoshida T; Mizukami T; Taya Y; Fujiwara T; Kato H; Saya H; Nakao M (Reprint)
CORPORATE SOURCE: Kumamoto Univ, Sch Med, Dept Tumor Genet & Biol, 2-2-1 Honjo, Kumamoto 8600811, Japan (Reprint); Kumamoto Univ, Sch Med, Dept Tumor Genet & Biol, Kumamoto 8600811, Japan; Kurume Univ, Sch Med, Dept Pediat & Child Hlth, Kurume, Fukuoka 8300011, Japan; Kyowa Hakko Kogyo Co Ltd, Tokyo Res Labs, Tokyo 1940023, Japan; Ctr Canc, Res Inst, Chuo Ku, Tokyo 1040045, Japan; Okayama Univ, Sch Med, Dept Surg 1, Okayama 7000914, Japan
COUNTRY OF AUTHOR: Japan
SOURCE: ONCOGENE, (28 OCT 1999) Vol. 18, No. 44, pp. 6037-6049.
ISSN: 0950-9232.
PUBLISHER: NATURE PUBLISHING GROUP, HOUNDMILLS, BASINGSTOKE RG21 6XS, HAMPSHIRE, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 53
ENTRY DATE: Entered STN: 1999
Last Updated on STN: 1999
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Mutant-type p53 (mt p53) is largely accumulated in cancer cells due to its increased stability, To elucidate the mechanism of mt p53 stabilization, we analysed the turnover of p53 mutated at codon 248 whose alteration is most frequently found in human cancers. Proteasome inhibition induced the accumulation of ubiquitinated mt p53, indicating that the ubiquitinated forms were essentially unstable and degraded by the proteasome, The presence of a small amount of the ubiquitinated mt p53 relative to the abundant non-ubiquitinated form suggested that the mt p53 ubiquitination was a rate-limiting process in the slow turnover, Two phenomena destabilizing mt p53 via the ubiquitin-proteasome degradation were proved to be independent, First, the coexpression of wild-type p53 (wt p53) promoted mt p53 destabilization as feedback regulation. Second, geldanamycin also induced mt p53 destabilization through the dissociation of the protein from hsp90 but not through the restoration of wt p53 function. Neither the mutant-specific conformation nor the N-terminal phosphorylation seemed to contribute directly to the mt p53 stabilization, Further, a two-dimensional gel electrophoresis revealed that most of the post-translationally modified mt p53 was equally subjected to ubiquitination and subsequent proteasomal degradation, These findings are evidence that mt p53 stabilization depends on the impaired ubiquitination due to both the loss of wt p53 function and the hsp90 association.

L30 ANSWER 12 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1999:273962 SCISEARCH Full-text
THE GENUINE ARTICLE: 184DT
TITLE: Definition of a p53 transactivation function-deficient mutant and characterization of two independent p53 transactivation subdomains
AUTHOR: Venot C; Maratrat M; Sierra V; Conseiller E; Debussche L (Reprint)
CORPORATE SOURCE: Rhone Poulenc Rorer, Ctr Rech Vitry Alfortville, 13 Quai Jules Guesde, F-94403 Vitry, France (Reprint); Rhone Poulenc Rorer, Ctr Rech Vitry Alfortville, F-94403 Vitry, France
COUNTRY OF AUTHOR: France
SOURCE: ONCOGENE, (8 APR 1999) Vol. 18, No. 14, pp. 2405-2410. ISSN: 0950-9232.
PUBLISHER: NATURE PUBLISHING GROUP, HOUNDMILLS, BASINGSTOKE RG21 6XS, HAMPSHIRE, ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 47
ENTRY DATE: Entered STN: 1999
Last Updated on STN: 1999
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The wild-type protein product of the p53 tumor suppressor gene can activate transcription of genes which are involved in mediating either growth arrest, e.g. WAF1 or apoptotis, e.g. BAX and PIG3. Additionally, p53 can repress a variety of promoters, which, in turn, may be responsible for the functional activities exhibited by p53. This study shows that the Q22, S23 double mutation, which is known to inactivate a p53 transactivation subdomain located within the initial 40 residues of the protein, while abrogating transactivation from the WAF1 promoter, only attenuates apoptosis triggering, transactivation from other p53-responsive promoters and repression of promoters by p53. The Q53, S54 double mutation, which inactivates another p53 transactivation subdomain situated between amino acids 43 and 73 results in attenuation of all of the aforementioned p53 activities. In contrast to the Q22, S23 double mutation, this latter mutation set does not alter mdm-2-mediated inhibition and degradation of p53. Finally, mutation of all four residues results in complete abrogation of every p53 activity mentioned above.

L30 ANSWER 13 OF 22 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 1999:936763 SCISEARCH Full-text
THE GENUINE ARTICLE: 261DK
TITLE: Hydrophobicity at the surface of proteins
AUTHOR: Scarsi M; Majeux N; Caflisch A (Reprint)
CORPORATE SOURCE: Univ Zurich, Dept Biochem, Winterthurerstr 190, CH-8057 Zurich, Switzerland (Reprint); Univ Zurich, Dept Biochem, CH-8057 Zurich, Switzerland
COUNTRY OF AUTHOR: Switzerland
SOURCE: PROTEINS-STRUCTURE FUNCTION AND GENETICS, (1 DEC 1999) Vol. 37, No. 4, pp. 565-575. ISSN: 0887-3585.
PUBLISHER: WILEY-LISS, DIV JOHN WILEY & SONS INC, 605 THIRD AVE, NEW YORK, NY 10158-0012 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 62
ENTRY DATE: Entered STN: 1999
Last Updated on STN: 1999
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Anew method is presented to quantitatively estimate and graphically display the propensity of nonpolar groups to bind at the surface of proteins.:It is based on the calculation of the binding energy, i.e., van der Waals interaction plus protein electrostatic desolvation, of a nonpolar probe sphere rolled over the protein surface, and on the color coding of this quantity on a smooth molecular surface (hydrophobicity map), The method is validated on ten protein-ligand complexes and is shown to distinguish precisely where polar and nonpolar groups preferentially bind. Comparisons with existing approaches, like the display of the electrostatic potential or the curvature, illustrate the advantages and the better predictive

```
             power of the present method.  Hydrophobicity maps will play an important role in
             the characterization of binding sites for the large number of proteins emerging
             from the genome projects and structure modeling approaches.  Proteins 1999;37:565-
             575, (C) 1999 Wiley-Liss, Inc.


L30  ANSWER 14 OF 22  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:     1999:644571  SCISEARCH Full-text
THE GENUINE ARTICLE: 230QE
TITLE:                Novel phosphorylation sites of human tumour suppressor
                      protein p53 at Ser(20) and Thr(18) that disrupt the
                      binding of mdm2 (mouse double minute 2) protein
                      are modified in human cancers
AUTHOR:               Craig A L; Burch L; Vojtesek B; Mikutowska J; Thompson A;
                      Hupp T R (Reprint)
CORPORATE SOURCE:     Univ Dundee, Ninewells Med Sch, Dept Mol & Cellular
                      Pathol, Dundee DD1 9SY, Scotland (Reprint); Univ Dundee,
                      Ninewells Med Sch, Dept Mol Oncol, Dundee DD1 9SY,
                      Scotland; Masaryk Mem Canc Inst, Dept Cellular & Mol
                      Oncol, Brno 65653, Czech Republic; Univ Dundee, Ninewells
                      Med Sch, Dundee Canc Inst, Dept Surg, Dundee DD1 9SY,
                      Scotland
COUNTRY OF AUTHOR:    Scotland; Czech Republic
SOURCE:               BIOCHEMICAL JOURNAL, (15 AUG 1999) Vol. 342, Part 1, pp.
                      133-141.
                      ISSN: 0264-6021.
PUBLISHER:            PORTLAND PRESS, 59 PORTLAND PLACE, LONDON W1N 3AJ, ENGLAND

DOCUMENT TYPE:        Article; Journal
LANGUAGE:             English
REFERENCE COUNT:      50
ENTRY DATE:           Entered STN: 1999
                      Last Updated on STN: 1999
                     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB           The ability to separate the isoforms of human tumour suppressor protein p53
             expressed in insect cells using heparin-Sepharose correlates with differences in
             the isoelectric point of p53, demonstrating that p53 can be heterogeneously
             modified and providing support for the use of insect cells as a model system for
             identifying novel signalling pathways that target p53, One p53 isoform that was
             reduced in its binding to the monoclonal antibody DO-1 could be stimulated in its
             binding to DO-1 by prior incubation with protein phosphatases, suggesting the
             presence of a previously unidentified N-terminal phosphorylation site capable of
             masking the DO-1 epitope, A synthetic peptide from the N-terminal domain of p53
             containing phosphate at Ser(20) inhibited DO-1 binding, thus identifying the
             phosphorylation site responsible for DO-1 epitope masking.  Monoclonal antibodies
             overlapping the DO-1 epitope were developed that are specific for phospho-Thr(18)
             (adjacent to the DO-1 epitope) and phospho-Ser(20) (within the DO-1 epitope) to
             determine whether direct evidence could be obtained for novel phosphorylation sites
             in human p53.  A monoclonal antibody highly specific for phospho-Ser(20) detected
             significant phosphorylation of human p53 expressed in insect cells, whereas the
             relative proportion of p53 modified at Thr(18) was substantially lower. The
             relevance of these two novel phosphorylation sires to p53 regulation in human cells
             was made evident by the extensive phosphorylation of human p53 at Thr(18) and
             Ser(20) in a panel of human breast cancers with a wild-type p53 status.  Phospho-
             Ser(20) or phospho-Thr(18) containing p53 peptides are as effective as the phospho-
             Ser(15) peptide at reducing mdm2 (mouse double minute 2) protein binding,
             indicating that the functional effects of these phosphorylation events might be to
             regulate the binding of heterologous proteins to p53, These results provide
             evidence in vivo for two novel phosphorylation sites within p53 at Ser(20) and
             Thr(18) that can affect p53 protein-protein interactions and indicate that some
             human cancers might have amplified one or more Ser(20) and Thr(18) kinase
             signalling cascades to modulate p53 activity.


L30  ANSWER 15 OF 22  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:     1998:882406  SCISEARCH Full-text
THE GENUINE ARTICLE: 139BE
TITLE:                Structure and specificity of nuclear receptor-coactivator
                      interactions
```

```
AUTHOR:               Darimont B D; Wagner R L; Apriletti J W; Stallcup M R;
                      Kushner P J; Baxter J D; Fletterick R J; Yamamoto K R
                      (Reprint)
CORPORATE SOURCE:     Univ Calif San Francisco, Dept Mol & Cellular Pharmacol,
                      San Francisco, CA 94143 USA (Reprint); Univ Calif San
                      Francisco, Grad Grp Biophys, San Francisco, CA 94143 USA;
                      Univ Calif San Francisco, Dept Biochem & Biophys, San
                      Francisco, CA 94143 USA; Univ Calif San Francisco, Metab
                      Res Unit, San Francisco, CA 94143 USA; Univ So Calif, Dept
                      Pathol, Los Angeles, CA 90033 USA
COUNTRY OF AUTHOR:    USA
SOURCE:               GENES & DEVELOPMENT, (1 NOV 1998) Vol. 12, No. 21, pp.
                      3343-3356.
                      ISSN: 0890-9369.
PUBLISHER:            COLD SPRING HARBOR LAB PRESS, 1 BUNGTOWN RD, PLAINVIEW, NY
                      11724 USA.
DOCUMENT TYPE:        Article; Journal
LANGUAGE:             English
REFERENCE COUNT:      53
ENTRY DATE:           Entered STN: 1998
                      Last Updated on STN: 1998
                     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB             Combinatorial regulation of transcription implies flexible yet precise assembly of
               multiprotein regulatory complexes in response to signals.  Biochemical and
               crystallographic analyses revealed that hormone binding leads to the formation of a
               hydrophobic groove within the ligand binding domain (LBD) of the thyroid hormone
               receptor that interacts with an LxxLL motif-containing alpha-helix from GRIP1, a
               coactivator.  Residues immediately adjacent to the motif modulate the affinity of
               the interaction; the motif and the adjacent sequences are employed to different
               extents in binding to different receptors.  Such interactions of amphipathic alpha-
               helices with hydrophobic grooves define protein interfaces in other regulatory
               complexes as well.  We suggest that these common structural elements impart
               flexibility to combinatorial regulation, whereas side chains at the interface
               impart specificity.


L30  ANSWER 16 OF 22  BIOSIS  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:    1999:112126  BIOSIS Full-text
DOCUMENT NUMBER:     PREV199900112126
TITLE:               Negative control elements of the cell cycle in human
                     tumors.
AUTHOR(S):           Adams, Peter D. [Reprint author]; Kaelin, William G., Jr.
CORPORATE SOURCE:    Fox Chase Cancer Center, 7701 Burholme Avenue,
                     Philadelphia, PA 19104, USA
SOURCE:              Current Opinion in Cell Biology, (Dec., 1998) Vol. 10, No.
                     6, pp. 791-797. print.
                     CODEN: COCBE3. ISSN: 0955-0674.
DOCUMENT TYPE:       Article
                     General Review; (Literature Review)
LANGUAGE:            English
ENTRY DATE:          Entered STN: 12 Mar 1999
                     Last Updated on STN: 12 Mar 1999

L30  ANSWER 17 OF 22  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:     1998:61389  SCISEARCH Full-text
THE GENUINE ARTICLE: YQ513
TITLE:                CTS1: A p53-derived chimeric tumor suppressor gene with
                      enhanced in vitro apoptotic properties
AUTHOR:               Conseiller E; Debussche L; Landais D; Venot C; Maratrat M;
                      Sierra V; Tocque B; Bracco L (Reprint)
CORPORATE SOURCE:     Rhone Poulenc Rorer SA, Gene Med Dept, 13 Quai Jules
                      Guesde, F-94403 Vitry Sur Seine, France (Reprint); Rhone
                      Poulenc Rorer SA, Gene Med Dept, F-94403 Vitry Sur Seine,
                      France
COUNTRY OF AUTHOR:    France
SOURCE:               JOURNAL OF CLINICAL INVESTIGATION, (1 JAN 1998) Vol. 101,
                      No. 1, pp. 120-127.
                      ISSN: 0021-9738.
PUBLISHER:            AMER SOC CLINICAL INVESTIGATION INC, 35 RESEARCH DR, STE
```

```
                      300, ANN ARBOR, MI 48103 USA.
DOCUMENT TYPE:        Article; Journal
LANGUAGE:             English
REFERENCE COUNT:      49
ENTRY DATE:           Entered STN: 1998
                      Last Updated on STN: 1998
                     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB                  The clinical potential of the p53 tumor suppressor gene is being evaluated
                    currently for gene therapy of cancer.  We have built a variant of wild-type p53,
                    chimeric tumor suppressor 1 (CTS1), in which we have replaced the domains that
                    mediate its inactivation.  CTS1 presents some very interesting properties: (a)
                    enhanced transcriptional activity; (b) resistance to the inactivation by oncogenic
                    forms of p53; (c) resistance to the inactivation by MDM2; (d) lower sensitivity to
                    E6-induced degradation; (e) ability to suppress cell growth; and (f) faster
                    induction of apoptosis.  Thus, CTS1 is an improved tumor suppressor and an
                    alternative for the treatment of wild-type p53-resistant human tumors by gene
                    therapy.

L30  ANSWER 18 OF 22     MEDLINE on STN              DUPLICATE 4
ACCESSION NUMBER:     97366808      MEDLINE Full-text
DOCUMENT NUMBER:      PubMed ID: 9223638
TITLE:                Molecular characterization of the hdm2-p53
                      interaction.
AUTHOR:               Bottger A; Bottger V; Garcia-Echeverria C; Chene P;
                      Hochkeppel H K; Sampson W; Ang K; Howard S F; Picksley S M;
                      Lane D P
CORPORATE SOURCE:     Cancer Research Campaign Laboratories, University of
                      Dundee, Scotland, UK.
SOURCE:               Journal of molecular biology, (1997 Jun 27) Vol. 269, No.
                      5, pp. 744-56.
                      Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY:         ENGLAND: United Kingdom
DOCUMENT TYPE:        Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:             English
FILE SEGMENT:         Priority Journals
ENTRY MONTH:          199708
ENTRY DATE:           Entered STN: 25 Aug 1997
                      Last Updated on STN: 6 Feb 1998
                      Entered Medline: 13 Aug 1997
AB      A number of viral oncogenes target the tumour suppressor protein p53 and inactivate its
        function.  This is an important step in tumourogenesis. The cellular oncogene hdm2 acts
        through a similar mechanism.  It binds the N terminus of p53, thereby interfering with the
        ability of p53 transcriptionally to activate genes responsible for growth arrest or
        apoptosis after genotoxic insults.  The disruption of the interaction of the two proteins
        therefore comprises a promising therapeutic target for treatment of the subset of human
        cancers in which this pathway is active. In this paper we attempt to characterize the p53-
        hdm2 interaction biochemically.  We analyse the potential of a series of peptide
        inhibitors, derived from previously described mdm2 binding peptide display phage, to
        disrupt this interaction in ELISA assays.  We conclude that F19, W23 and L26 of p53 are
        critical contact points for p53 binding to hdm2.  Furthermore, we show the potential of
        the monoclonal antibody 3G5 to interfere with binding of p53 to hdm2 in ELISA assays.
        Consequently, we define the binding site of 3G5 on hdm2 using overlapping peptides derived
        from the N terminus of hdm2 and phage display libraries.  The result indicates L66, Y67
        and E69 on hdm2 as critical binding points for 3G5.  In electrophoretic mobility shift
        assay we demonstrate the formation of hdm2-p53 complexes that can be disrupted in the
        presence of 3G5 or inhibitory peptides.  Finally, we describe the effects of NEM and DTT
        on the interaction between the two molecules in ELISA assays.  All our results are
        discussed in the light of the recently published crystal structure of the mdm2-p53
        complex. A striking correspondence between our findings and the crystal structure is
        revealed.

L30  ANSWER 19 OF 22     MEDLINE on STN              DUPLICATE 5
ACCESSION NUMBER:     97278280      MEDLINE Full-text
DOCUMENT NUMBER:      PubMed ID: 9131587
TITLE:                A genetic approach to mapping the p53 binding site in the
                      MDM2 protein.
AUTHOR:               Freedman D A; Epstein C B; Roth J C; Levine A J
CORPORATE SOURCE:     Department of Molecular Biology, Princeton University, NJ
                      08544-1014, USA.
```

CONTRACT NUMBER: 5T326M07312 (NCI)
P01CA41086
SOURCE: Molecular medicine (Cambridge, Mass.), (1997 Apr) Vol. 3, No. 4, pp. 248-59.
Journal code: 9501023. ISSN: 1076-1551.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 30 Jun 1997
Last Updated on STN: 30 Jun 1997
Entered Medline: 18 Jun 1997

AB BACKGROUND: The MDM2 oncoprotein binds to the tumor suppressor p53 and inhibits its anti-oncogenic functions. MATERIALS AND METHODS: To determine the amino acids of MDM2 that are critical for binding to p53, a modified two-hybrid screen was performed in yeast. Site-directed mutagenesis was then performed to identify MDM2 residues important for p53 interaction. Mutant MDM2 proteins were subsequently tested for their ability to bind to p53 in vitro and for their ability to regulate p53-mediated transcription in vivo. RESULTS: The yeast genetic screen yielded two Mdm2 mutations (G58D and C77Y) which disrupted binding to p53 in vitro without altering the conformation of MDM2 as determined with conformation-sensitive monoclonal antibodies. Site-directed mutagenesis yielded mutations of two additional amino acids of MDM2 (D68 and V75) that prevented binding to p53 in vitro. The mutant MDM2 proteins were unable to inhibit p53-dependent transcription in vivo, which is consistent with prior indications that a physical interaction between the two proteins is required for MDM2's inhibition of p53. Finally, the crystal structure of the MDM2-p53 complex shows that two of the four critical residues identified here contact p53 directly, while the remaining two residues play important structural roles in the MDM2 domain. CONCLUSIONS: MDM2 residues G58, D68, V75, and C77 are critical for MDM2's interaction with the p53 protein. Mutation of these residues to alanine prevents MDM2's interaction with p53 in vitro, and MDM2's regulation of p53's transcriptional activity in vivo.

L30 ANSWER 20 OF 22 MEDLINE on STN
ACCESSION NUMBER: 97081050 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 8875929
TITLE: Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor transactivation domain.
AUTHOR: Kussie P H; Gorina S; Marechal V; Elenbaas B; Moreau J; Levine A J; Pavletich N P
CORPORATE SOURCE: Cellular Biochemistry and Biophysics Program, Memorial Sloan-Kettering Cancer Center, New York, NY 10021, USA.. nikola@xray2.mskcc.org
CONTRACT NUMBER: CA65698 (NCI)
SOURCE: Science, (1996 Nov 8) Vol. 274, No. 5289, pp. 948-53.
Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Commentary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-1YCQ; PDB-1YCR
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 28 Jan 1997
Last Updated on STN: 28 Jan 1997
Entered Medline: 6 Dec 1996

AB The MDM2 oncoprotein is a cellular inhibitor of the p53 tumor suppressor in that it can bind the transactivation domain of p53 and downregulate its ability to activate transcription. In certain cancers, MDM2 amplification is a common event and contributes to the inactivation of p53. The crystal structure of the 109-residue amino-terminal domain of MDM2 bound to a 15-residue transactivation domain peptide of p53 revealed that MDM2 has a deep hydrophobic cleft on which the p53 peptide binds as an amphipathic alpha helix. The interface relies on the steric complementarity between the MDM2 cleft and the hydrophobic face of the p53 alpha helix and, in particular, on a triad of p53 amino acids-Phe19, Trp23, and Leu26-which insert deep into the MDM2 cleft. These same p53 residues are also involved in transactivation, supporting the hypothesis that MDM2 inactivates p53 by concealing its transactivation domain. The structure also suggests that the amphipathic alpha helix may be a common structural motif in the binding of a diverse family of transactivation factors to the TATA-binding protein-associated factors.

```
L30  ANSWER 21 OF 22  CAPLUS  COPYRIGHT 2006 ACS on STN DUPLICATE 6
ACCESSION NUMBER:         1996:676457  CAPLUS Full-text
DOCUMENT NUMBER:          125:321010
TITLE:                    Structure of the MDM2 oncoprotein bound to
                          the p53 tumor suppressor transactivation domain
AUTHOR(S):                Kussie, Paul H.; Gorina, Svetlana; Marechal, Vincent;
                          Elenbaas, Brian; Moreau, Jacque; Levine, Arnold J.;
                          Pavletich, Nikola P.
CORPORATE SOURCE:         Cellular Biochemistry and Biophysics Program, Memorial
                          Sloan-Kettering Cancer Center, New York, NY, 10021,
                          USA
SOURCE:                   Science (Washington, D. C.) (1996), 274(5289), 948-953
                          CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER:                American Association for the Advancement of Science
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB     The MDM2 oncoprotein is a cellular inhibitor of the p53 tumor suppressor in that it can
       bind the transactivation domain of p53 and downregulate its ability to activate
       transcription.  In certain cancers, MDM2 amplification is a common event and contributes
       to the inactivation of p53.  The crystal structure of the 109-residue amino-terminal
       domain of MDM2 bound to a 15-residue transactivation domain peptide of p53 revealed that
       MDM2 has a deep hydrophobic cleft on which the p53 peptide binds as an amphipathic α
       helix.  The interface relies on the steric complementarity between the MDM2 cleft and the
       hydrophobic face of the p53 α helix and, in particular, on a triad of p53 amino acids -
       Phe19, Trp23, and Leu26 - which insert deep into the MDM2 cleft.  These same p53 residues
       are also involved in transactivation, supporting the hypothesis that MDM2 inactivates p53
       by concealing its transactivation domain.  The structure also suggests that the
       amphipathic α helix may be a common structural motif in the binding of a diverse family of
       transactivation factors to the TATA-binding protein-associated factors.


L30  ANSWER 22 OF 22      MEDLINE on STN
ACCESSION NUMBER:     95210372      MEDLINE Full-text
DOCUMENT NUMBER:      PubMed ID: 7696367
TITLE:                The tumor suppressor protein p53: a receptor to genotoxic
                      stress that controls cell growth and survival.
AUTHOR:               Hainaut P
CORPORATE SOURCE:     University of York, Heslington.
SOURCE:               Current opinion in oncology, (1995 Jan) Vol. 7, No. 1, pp.
                      76-82.  Ref: 58
                      Journal code: 9007265. ISSN: 1040-8746.
PUB. COUNTRY:         United States
DOCUMENT TYPE:        Journal; Article; (JOURNAL ARTICLE)
                      General Review; (REVIEW)
LANGUAGE:             English
FILE SEGMENT:         Priority Journals
ENTRY MONTH:          199505
ENTRY DATE:           Entered STN: 10 May 1995
                      Last Updated on STN: 10 May 1995
                      Entered Medline: 2 May 1995
AB     The p53 protein is a transcription regulator that is frequently altered by mutation in
       cancer.  Breakthroughs on two fronts shed light on its role in tumor suppression.  First,
       a flurry of biochemical and structural studies (including a partial crystal structure) has
       sharpened the picture of p53 topology and functional properties.  Second, downstream
       effectors of p53 have been identified including p21Waf-1/Cip-1, an inhibitor of cyclin-
       dependent kinases, and bax, a dominant-negative inhibitor of bcl-2.  This suggest a
       scenario in which p53 is activated by genotoxic stress and regulates the transcription of
       at least two sets of genes.  One is responsible for transient cell arrest in G1 and the
       other controls the initiation of apoptosis.  Both processes eliminate potential oncogenic
       mutations, either by proper DNA repair or by inducing damaged cells to commit suicide.



=> log y
```

Hit List

First Hit [Clear] [Generate Collection] [Print] [Fwd Refs] [Bkwd Refs]
[Generate OACS]

Search Results - Record(s) 1 through 9 of 9 returned.

☐ 1. Document ID: US 6965850 B2

Using default format because multiple data bases are involved.

L2: Entry 1 of 9 File: USPT Nov 15, 2005

US-PAT-NO: 6965850
DOCUMENT-IDENTIFIER: US 6965850 B2

TITLE: Methods for modulating nuclear receptor coactivator binding

DATE-ISSUED: November 15, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Baxter; John D.	San Francisco	CA		
Darimont; Beatrice	San Francisco	CA		
Feng; Weijun	San Francisco	CA		
Fletterick; Robert J.	San Francisco	CA		
Kushner; Peter J.	San Francisco	CA		
Wagner; Richard L.	San Francisco	CA		
West; Brian L.	San Francisco	CA		
Yamamoto; Keith R.	San Francisco	CA		

US-CL-CURRENT: 703/11; 257/E21.218, 257/E21.266, 435/7.1, 702/27, 703/2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 2. Document ID: US 6946259 B2

L2: Entry 2 of 9 File: USPT Sep 20, 2005

US-PAT-NO: 6946259
DOCUMENT-IDENTIFIER: US 6946259 B2

TITLE: Compositions and methods for treating cells having double minute DNA

DATE-ISSUED: September 20, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wahl; Geoffrey M.	San Diego	CA		

Shimizu; Noriaki	Hiroshima			JP
Kanda; Teru	La Jolla	CA		
Shepard; H. Michael	Rancho Santa Fe	CA		

US-CL-CURRENT: 435/7.8; 435/4, 435/40.5, 435/6, 435/7.1, 436/63, 436/64, 530/358

ABSTRACT:

This invention provides methods by which test substances can be screened for their ability to inhibit, enhance or eliminate double minute (DM) or extrachromosomal DNA by micronucleation in cells. This invention also provides a method for inducing maturation or death of a cell having the capacity to generate micronuclei. It also provides a method of treating a disease in a subject, the cells correlated with the disease having DM and extrachromosomal DNA as well as the capacity to generate micronuclei to capture them. Further provided is a method of detecting chromosomal and extrachromosomal DNA in a cell.

17 Claims, 41 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 14

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KMC | Draw. D

☐ 3. Document ID: US 6919178 B2

L2: Entry 3 of 9 File: USPT Jul 19, 2005

US-PAT-NO: 6919178
DOCUMENT-IDENTIFIER: US 6919178 B2

TITLE: Extended tethering approach for rapid identification of ligands

DATE-ISSUED: July 19, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Erlanson; Daniel A.	San Francisco	CA		
Braisted; Andrew C.	San Francisco	CA		
McDowell; Robert	San Francisco	CA		
Prescott; John	San Francisco	CA		

US-CL-CURRENT: 435/6; 435/4, 435/7.1

ABSTRACT:

The invention concerns a method for rapid identification and characterization of binding partners for a target molecule, and for providing binding partners with improved binding affinity. More specifically, the invention concerns an improved tethering method for the rapid identification of at least two binding partners that bind near one another to a target molecule.

27 Claims, 6 Drawing figures

Exemplary Claim Number: 1
Number of Drawing Sheets: 6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 4. Document ID: US 6911538 B2

L2: Entry 4 of 9 File: USPT Jun 28, 2005

US-PAT-NO: 6911538
DOCUMENT-IDENTIFIER: US 6911538 B2

TITLE: Engineered open reading frame for p53

DATE-ISSUED: June 28, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Brachmann; Rainer K.	St. Louis	MO		

US-CL-CURRENT: 536/23.1; 536/24.3

ABSTRACT:

The transcription factor and tumor suppressor protein p53 is inactivated in many human cancers. Approximately forty percent of cancers carry large amounts of mutated full-length p53 protein with one of over 900 reported single amino acid changes in the p53 core domain that recognizes p53 DNA binding sites. The ability to restore function to these inactive p53 proteins would dramatically improve cancer therapy. Alternative open reading frames that are more easily engineered encode a wild-type p53. The alternative open reading frames are optimized for codon usage and expression of p53 proteins in E. coli, yeast and mammalian cells. The alternative open reading frames may additionally contain mutations that are naturally found in human cancers, substitutions that correspond to polymorphic p53 alleles, or mutations in residues that can be post-translationally modified.

2 Claims, 7 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 5. Document ID: US 6767541 B2

L2: Entry 5 of 9 File: USPT Jul 27, 2004

US-PAT-NO: 6767541
DOCUMENT-IDENTIFIER: US 6767541 B2

TITLE: HER-2/neu overexpression abrogates growth inhibitory pathways

DATE-ISSUED: July 27, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Slamon; Dennis J.	Woodland Hills	CA		
Wilson; Cindy A.	Los Angeles	CA		
Calzone; Frank J.	Westlake Village	CA		

US-CL-CURRENT: 424/143.1; 424/130.1, 424/133.1, 424/141.1, 424/142.1, 424/152.1, 424/155.1, 424/156.1, 424/172.1, 424/174.1, 514/2, 530/387.1, 530/387.3, 530/387.7, 530/388.1, 530/388.15, 530/388.2, 530/388.22, 530/388.8, 530/388.85

ABSTRACT:

The present invention provides methods for obtaining genetic profiles of cancer cells in order to assess the status of a cancer in an individual. In addition, the present invention provides methods for inhibiting the growth of cancer cells that exhibit certain genetic profiles. These methods identify an important link between HER-2/neu overexpression and loss of growth inhibition by the TGF-.beta. signaling pathway in cancer cells. Compositions as well as therapeutic and diagnostic methodologies based on this disclosure are provided.

19 Claims, 39 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 10

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 6. Document ID: US 6479285 B1

L2: Entry 6 of 9 File: USPT Nov 12, 2002

US-PAT-NO: 6479285
DOCUMENT-IDENTIFIER: US 6479285 B1
**** See image for Certificate of Correction ****

TITLE: p53 as a regulator of cell differentiation

DATE-ISSUED: November 12, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vize; Peter D.	Austin	TX		
Wallingford; John B.	Houston	TX		

US-CL-CURRENT: 435/377; 435/320.1, 435/325, 435/375, 435/455, 435/459, 435/461, 536/23.1, 536/23.5, 800/21, 800/23, 800/25

ABSTRACT:

The present invention involves the role of p53 in the differentiation of embryonic tissues. More particularly, the present invention provides methods of the blocking

of p53 function in embryonic tissues, and the use of these tissues as screening tools for substances that are capable of overcoming the p53-related block in differentation, both in vitro and in vivo. The similarities between undifferentiated embryonic cells and tumor cells is evident, and thus these assays serve as a model for possible cancer therapeutics. In addition, methods for identifying additional cellular components that interact p53 or p53-related pathways are provided.

13 Claims, 17 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 7. Document ID: US 6451979 B1

L2: Entry 7 of 9 File: USPT Sep 17, 2002

US-PAT-NO: 6451979
DOCUMENT-IDENTIFIER: US 6451979 B1

TITLE: Methods of treatment using NBS-1, antibodies and proteins thereto, and uses of the antibodies

DATE-ISSUED: September 17, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kaelin; William	Boston	MA		
Jost; Christine	Jamaica Plain	MA		

US-CL-CURRENT: 530/387.1; 435/810, 530/387.3, 530/388.1, 530/388.2, 530/388.8, 530/388.85

ABSTRACT:

Antibodies that will specifically bind to NBS-1 are described. It is also shown that NBS-1 will interact with p53 responsive elements in a p53 promoter. Thus, NBS-1 can be used in subjects having a p53-dependent tumor to inhibit growth of that tumor.

10 Claims, 39 Drawing figures
Exemplary Claim Number: 1,3
Number of Drawing Sheets: 20

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 8. Document ID: US 20050037383 A1

L2: Entry 8 of 9 File: DWPI Feb 17, 2005

DERWENT-ACC-NO: 2005-180390
DERWENT-WEEK: 200519
COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Novel modified human double minute 2 protein polypeptide, comprising amino acid sequence differing from its corresponding wild-type, useful for identifying compounds used as anticancer agents

INVENTOR: DUCA, J S; HESSON, T ; MADISON, V S ; REICHERT, P ; STRICKLAND, C ; TAREMI, S S ; WINDSOR, W T ; XIE, G ; ZHANG, R

PRIORITY-DATA: 2004US-0822254 (April 9, 2004), 2003US-461787P (April 10, 2003), 2004US-547265P (February 24, 2004)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 20050037383 A1	February 17, 2005		049	C12Q001/68

INT-CL (IPC): C07 H 21/04; C07 K 14/47; C12 Q 1/68

ABSTRACTED-PUB-NO: US20050037383A
BASIC-ABSTRACT:

NOVELTY - A modified human Double Minute 2 protein (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino acids (S1) as given in the specification, differing from the corresponding wild-type Hdm2 (17-125) amino acid sequence having a fully defined sequence of 109 amino acids (S2) as given in the specification, is new.

DETAILED DESCRIPTION - A modified human Double Minute 2 protein (Hdm2) polypeptide (I) comprises a fully defined sequence of 109 amino acids (S1) as given in the specification, where at least one of the seven variable positions of (S1) has an amino acid residue that differs from that of the corresponding wild-type Hdm2 (17-125) amino acid sequence having a fully defined sequence of 109 amino acids (S2) as given in the specification, and optionally comprises 1-10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of (S1).

INDEPENDENT CLAIMS are also included for the following:

(1) a nucleic acid (II) encoding (I);

(2) an expression vector (V1) comprising (II), and further comprising a transcriptional control sequence operatively linked to (II);

(3) a host cell (HC) comprising V1;

(4) producing (I);

(5) obtaining purified form of (I), involves purifying (I) produced in the culture medium, by cultivating HC in the culture medium;

(6) a compound (C1) chosen from any one of compound of formula (1);

(7) a polypeptide-compound complex (PPC) comprising (I) complexed to C1;

(8) a crystal (III) comprising (I), and having structure coordinates comprising a root mean square deviation (RMSD) of conserved residue backbone atoms described in structural coordinates (SC) of Hdm2 F55Y/Y76H-Tripeptide complex, or structural

coordinates (SC1) of Hdm2 Y76H-Tripeptide complex, as given in the specification;

(9) producing (M1) crystal of (I), involves providing (I), and incubating (I) under conditions in which (III) is formed;

(10) computer (IV) for producing a three-dimensional representation of (I) or PPC having RMSD from the backbone atoms of SC or SC1 of less than 2.0 Angstrom , comprising (a) machine-readable data storage medium comprising a data storage material encoded with machine-readable data, where the data comprises SC or SC1, (b) a working memory for storing instructions for processing the machine-readable data, (c) a central-processing unit coupled to the working memory and to the machine-readable data storage medium for processing the machine readable data into the three-dimensional representation, and (d) a display unit coupled to the central-processing unit for displaying the three-dimensional representation; and

(11) obtaining structural information concerning a molecule of unknown structure, involves generating X-ray diffraction data from a crystallized form of the molecule, and applying crystallographic phases derived from at least a portion of SC or SC1, to the X-ray diffraction pattern to generate a three-dimensional electron density map of at least a portion of the molecule.

X = Cl or Br.

USE - (I) is useful for identifying an agent for use as an inhibitor of Hdm2, which involves contacting the potential agent with (I) and p53 substrate, and determining the ability of (I) to bind to the p53 substrate, where a potential agent is identified as an agent that inhibits Hdm2 when there is a decrease in the binding of (I) and the p53 substrate in the presence of the agent relative to in its absence. (I), (III) or PPC is useful for designing, selecting and/or optimizing a potential inhibitor of (I), which involves (a) providing the structure coordinates of (I) or PPC, on a computer comprising the mode for generating three-dimensional structural information from the structure coordinates, and (b) designing, selecting and/or optimizing the potential inhibitor by performing a fitting operation between the potential inhibitor and the three-dimensional structural information of (I) or PPC. The method further involves providing or synthesizing the potential inhibitor, contacting the potential inhibitor with (I), and determining whether the potential inhibitor binds to (I) and inhibits its activity, where the structural coordinates include SC or SC1, or comprise RMSD of conserved residue backbone atoms of less than 1.5 Angstrom when superimposed on backbone described by SC or SC1. (I) or PPC is useful for evaluating the ability of a potential inhibitor to associate with (I) or PPC, which involves (a) employing computational unit to perform a fitting operation between the structural coordinates of the potential inhibitor and the structural coordinates of (I) or PPC, and analyzing the results of the fitting operation to quantitate the association between the potential inhibitor and (I) or PPC. The method further involves generating a three-dimensional graphical representation of (I) or PPC before employing computational unit to perform fitting operation, where the structural coordinates include SC or SC1, or comprise RMSD of conserved residue backbone atoms of less than 2.0 Angstrom when superimposed on backbone described by SC or SC1 (all claimed). (I), (III) or PPC is useful for identifying, selecting and/or designing compounds useful as anticancer agents. (I) is useful in designing high affinity inhibitors of Hdm2 that are useful in the treatment of cancers.

ADVANTAGE - (I) exhibits improved solubility and/or stability without compromising its ability to bind p53, and amenable to crystallization. (I) is soluble and stable at high protein concentrations even when a protein is free of p53 or its fragments.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 9. Document ID: WO 2005114173 A2, US 20040197893 A1

L2: Entry 9 of 9 File: DWPI Dec 1, 2005

DERWENT-ACC-NO: 2004-736286
DERWENT-WEEK: 200580
COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Crystal comprises human double minute 2 protein (HDM2), or fragment, or target structural motif or its derivative, and a ligand such as small molecular inhibitor, useful for identifying potential agonist or antagonist against HDM2

INVENTOR: DECKMAN, I; GRASBERGER, B ; MAGUIRE, D ; SCHUBERT, C ; SPURLINO, J

PRIORITY-DATA: 2002US-418350P (October 16, 2002), 2003US-0685838 (October 15, 2003), 2004WO-US12347 (April 22, 2004)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
WO 2005114173 A2	December 1, 2005	E	000	G01N031/00
US 20040197893 A1	October 7, 2004		076	G06F019/00

INT-CL (IPC): C12 N 9/64; G01 N 31/00; G01 N 33/48; G01 N 33/50; G06 F 19/00

ABSTRACTED-PUB-NO: US20040197893A
BASIC-ABSTRACT:

NOVELTY - A crystal (I) comprises (a) human double minute 2 protein (HDM2), or a fragment, or target structural motif or its derivative, and a ligand, where the ligand is a small molecular inhibitor, or (b) a sequence (S1) with amino acid residues 17-111 of a full length HDM2 sequence, and comprising an atomic structure characterized by the coordinates (C1) as given in the patent specification. Sequence listing not provided in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a computer system (II), comprising a database containing information on the three dimensional structure of a crystal comprising HDM2, or a fragment or a target structural motif or its derivative, and a ligand, where the ligand is a small molecule inhibitor, stored on a computer readable storage medium, and a user interface to view the information;

(2) evaluating (M1) the potential of an agent to associate with HDM2, involves exposing HDM2 to the agent, and detecting the association of the agent to HDM2 amino acid residues Ser17, Ile19, Leu82 and Arg97, thus evaluating the potential;

(3) evaluating (M2) the potential of an agent to associate with the peptide having amino acid16-(S1), involves exposing amino acid16-(S1) to the agent, and detecting the level of association of the agent to amino acid16-(S1), thus evaluating the potential;

(4) locating the attachment site of an inhibitor to HDM2, involves:

(i) obtaining X-ray diffraction data for a crystal of HDM2;

(ii) obtaining X-ray diffraction data for a complex of HDM2 and an inhibitor;

(iii) subtracting the X-ray diffraction data obtained in step (i) from the X-ray diffraction data obtained in step (ii) to obtain the difference in the X-ray diffraction data;

(iv) obtaining phases that correspond to X-ray diffraction data obtained in step (i);

(v) utilizing the phases obtained in step (iv) and the difference in the X-ray diffraction data obtained in step (iii) to compute a difference Fourier image of the inhibitor; and

(vi) locating the attachment site of the inhibitor to HDM2 based on the computations obtained in step (v);

(5) obtaining (M3) a modified inhibitor, involves obtaining a crystal comprising HDM2 and an inhibitor, obtaining the atomic coordinates of the crystal, using the atomic coordinates and one or more or more molecular modeling techniques to determine how to modify the interaction of the inhibitor with HDM2, and modifying the inhibitor based on the determinations obtained in the above step to produce a modified inhibitor;

(6) an HDM2 inhibitor identified by (M3);

(7) an isolated protein fragment (III) comprising a binding pocket or active site defined by structure coordinates of HDM2 amino acid residues Ser17, Ile19, Leu82, and Arg97;

(8) an isolated nucleic acid molecule (IV) encoding (III);

(9) a vector (V) comprising (IV);

(10) a host cell (VI) comprising (V);

(11) a kit comprising (III);

(12) producing (M4) a crystal complex comprising an HDM2 polypeptide-ligand, involves contacting the HDM2 polypeptide with the ligand in a suitable solution comprising polyethylene glycol (PEG) and NaSCN, and crystallizing the resulting complex of HDM2 polypeptide-ligand from the solution;

(13) producing (Ia), involves crystallizing a peptide comprising a full length amino acid sequence (S2) of HDM2, a sequence of (S1), a sequence (S3) having amino acid residues 23-114 of (S2), or a sequence (S4) having amino acids 16-111 of (S2) (Gly16-S1) with a potential inhibitor;

(14) identifying (M5) a potential inhibitor of HDM2, involves using a three dimensional structure of HDM2 as defined by (C1), replacing one or more HDM2 amino acids chosen from Ser17, Ile19, Leu82 and Arg97 in the three-dimensional structure with a different amino acid to produce a modified HDM2, using the three-dimensional structure to design or select the potential inhibitor, synthesizing the potential inhibitor, and contacting the potential inhibitor with the modified HDM2 in the presence of a substrate to test the ability of the potential inhibitor to inhibit HDM2 or the modified HDM2; and

(15) an inhibitor identified by (M5)

USE - (Ia) is useful for identifying a potential agonist or antagonist against HDM2, which involves employing the three dimensional structure of HDM2 co-crystallized with a small molecule inhibitor to design or select the potential agonist or antagonist. The three dimensional structure corresponds to the atomic structure characterized by (C1) or similar structure coordinates comprising a route mean square deviation of non-hydrogen atoms of less than about 1.5 Angstrom when super imposed on the non-hydrogen atom positions of the corresponding atomic coordinates of (C1). The method further involves synthesizing the potential agonist or antagonist and contacting the potential agonist or antagonist with HDM2. (III) is useful for screening for an agent that associates with HDM2, which involves exposing (III) to the agent, and detecting the level of association of the agent to the fragment. (VI) is useful for producing a protein fragment, which involves culturing (VI) under conditions in which the fragment is expressed (all claimed).

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Terms	Documents
(human double minute 2 protein or hdm2 or mdm2) same crystal	9

Display Format: - Change Format

Previous Page Next Page Go to Doc#

Hit List

First Hit Clear Generate Collection Print Fwd Refs Bkwd Refs Generate OACS

Search Results - Record(s) 1 through 20 of 20 returned.

☐ 1. Document ID: US 20060088847 A1

Using default format because multiple data bases are involved.

L3: Entry 1 of 20 File: PGPB Apr 27, 2006

PGPUB-DOCUMENT-NUMBER: 20060088847
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20060088847 A1

TITLE: ARF-BP1 as mediator of p53-dependent and independent tumor suppression and uses thereof

PUBLICATION-DATE: April 27, 2006

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Gu; Wei	Paramus	NJ	US

US-CL-CURRENT: 435/6; 435/226, 435/320.1, 435/325, 435/69.1, 435/7.23, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 2. Document ID: US 20060088836 A1

L3: Entry 2 of 20 File: PGPB Apr 27, 2006

PGPUB-DOCUMENT-NUMBER: 20060088836
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20060088836 A1

TITLE: Methods and compositions for diagnosing and monitoring transplant rejection

PUBLICATION-DATE: April 27, 2006

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Wohlgemuth; Jay	Menlo Park	CA	US
Fry; Kirk	Palo Alto	CA	US
Woodward; Robert	Pleasanton	CA	US
Ly; Ngoc	San Bruno	CA	US
Prentice; James	Austin	TX	US
Morris; MacDonald	Atherton	CA	US

Rosenberg; Steven	Oakland	CA	US

US-CL-CURRENT: 435/6; 435/91.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 3. Document ID: US 20050288287 A1

L3: Entry 3 of 20 File: PGPB Dec 29, 2005

PGPUB-DOCUMENT-NUMBER: 20050288287
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050288287 A1

TITLE: Chiral cis-imidazolines

PUBLICATION-DATE: December 29, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Fotouhi, Nader	Basking Ridge	NJ	US
Haley, Gregory Jay	San Diego	CA	US
Simonsen, Klaus B.	Frederiksberg	NJ	DK
Vu, Binh Thanh	North Caldwell	CA	US
Webber, Stephen Evan	San Diego		US

US-CL-CURRENT: 514/235.5; 514/254.05, 544/121, 544/370

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 4. Document ID: US 20050282803 A1

L3: Entry 4 of 20 File: PGPB Dec 22, 2005

PGPUB-DOCUMENT-NUMBER: 20050282803
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050282803 A1

TITLE: CIS-imidazolines

PUBLICATION-DATE: December 22, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Haley, Gregory Jay	San Diego	CA	US
Kong, Norman	West Caldwell	NJ	US
Liu, Emily Aijun	Burlingame	CA	US
Vu, Binh Thanh	North Caldwell	NJ	US

US-CL-CURRENT: 514/227.5; 514/235.5, 514/254.05, 514/326, 514/397, 544/139, 544/370, 544/60, 546/210, 548/311.1

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw. D

☐ 5. Document ID: US 20050227932 A1

L3: Entry 5 of 20 File: PGPB Oct 13, 2005

PGPUB-DOCUMENT-NUMBER: 20050227932
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050227932 A1

TITLE: Combinational therapy involving a small molecule inhibitor of the MDM2: p53 interaction

PUBLICATION-DATE: October 13, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Lu, Tianbao	Churchville	PA	US
Koblish, Holly K.	Exton	PA	US
Maroney, Anna	Media	PA	US

US-CL-CURRENT: 514/34; 514/221, 514/283, 514/49

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw. D

☐ 6. Document ID: US 20050215548 A1

L3: Entry 6 of 20 File: PGPB Sep 29, 2005

PGPUB-DOCUMENT-NUMBER: 20050215548
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050215548 A1

TITLE: Bisarylsulfonamide compounds and their use in cancer therapy

PUBLICATION-DATE: September 29, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Wang, Shudong	Angus		GB
Gibson, Darren	Dundee		GB
Duncan, Kenneth	Stirlingshire		GB
Bailey, Kevin	Derbyshire		GB
Thomas, Mark	Dundee		GB
MacCallum, David	By Forfar		GB
Zheleva, Daniella I.	Fife		GB
Turner, Nicholas John	Edinburgh		GB
Fischer, Peter Martin	Arbroath		GB

US-CL-CURRENT: 514/235.2; 514/322, 514/323, 514/338, 514/366, 514/406, 514/414

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 7. Document ID: US 20050186630 A1

L3: Entry 7 of 20 File: PGPB Aug 25, 2005

PGPUB-DOCUMENT-NUMBER: 20050186630
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050186630 A1

TITLE: Extended tethering approach for rapid identification of ligands

PUBLICATION-DATE: August 25, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Erlanson, Daniel A.	San Francisco	CA	US
Braisted, Andrew C.	San Francisco	CA	US
McDowell, Robert	San Francisco	CA	US
Prescott, John	San Francisco	CA	US

US-CL-CURRENT: 435/6; 435/7.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 8. Document ID: US 20050176075 A1

L3: Entry 8 of 20 File: PGPB Aug 11, 2005

PGPUB-DOCUMENT-NUMBER: 20050176075
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050176075 A1

TITLE: Mdm2 splice variants

PUBLICATION-DATE: August 11, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Jones, Stephen N.	Shrewsbury	MA	US
Steinman, Heather	North Grafton	MA	US

US-CL-CURRENT: 435/7.23; 435/320.1, 435/325, 435/69.3, 530/350, 530/388.8, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 9. Document ID: US 20050147608 A1

L3: Entry 9 of 20 File: PGPB Jul 7, 2005

PGPUB-DOCUMENT-NUMBER: 20050147608
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050147608 A1

TITLE: Novel regulatory mechanisms of NF-kappaB

PUBLICATION-DATE: July 7, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Ryo, Akihide	Yokohama	MA	JP
Lu, Kun Ping	Newton		US

US-CL-CURRENT: 424/145.1; 435/226, 435/320.1, 435/325, 435/69.1, 514/44

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 10. Document ID: US 20050037383 A1

L3: Entry 10 of 20 File: PGPB Feb 17, 2005

PGPUB-DOCUMENT-NUMBER: 20050037383
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050037383 A1

TITLE: Soluble, stable form of HDM2, crystalline forms thereof and methods of use thereof

PUBLICATION-DATE: February 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Taremi, Shahriar Shane	Upper Montclair	NJ	US
Xie, Gaolian	Edison	NJ	US
Hesson, Thomas	Kendall Park	NJ	US
Duca, Jose S.	Cranford	NJ	US
Strickland, Corey	Martinsville	NJ	US
Windsor, William T.	East Brunswick	NJ	US
Madison, Vincent S.	Mountain Lakes	NJ	US
Zhang, Rumin	Edison	NJ	US
Reichert, Paul	Montville	NJ	US

US-CL-CURRENT: 435/6; 435/320.1, 435/325, 435/69.1, 530/350, 536/23.5

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 11. Document ID: US 20040220179 A1

L3: Entry 11 of 20 File: PGPB Nov 4, 2004

PGPUB-DOCUMENT-NUMBER: 20040220179
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040220179 A1

TITLE: Substituted 1,4-diazepines and uses thereof

PUBLICATION-DATE: November 4, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Lu, Tianbao	Churchville	PA	US
Milkiewicz, Karen L.	Exton	PA	US
Raboisson, Pierre	Mechelen	PA	BE
Cummings, Maxwell David	Wayne	PA	US
Calvo, Raul R.	Royersford	PA	US
Parks, Daniel J.	Downingtown	PA	US
Lafrance, Louis V. III	West Chester	PA	US
Marugan Sanchez, Juan Jose	Downingtown	PA	US
Gushue, Joan	Conshohocken	PA	US
Leonard, Kristi	West Chester		US

US-CL-CURRENT: 514/217.03; 514/221, 540/507

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. De

---

☐ 12. Document ID: US 20040197893 A1

L3: Entry 12 of 20 File: PGPB Oct 7, 2004

PGPUB-DOCUMENT-NUMBER: 20040197893
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040197893 A1

TITLE: HDM2-inhibitor complexes and uses thereof

PUBLICATION-DATE: October 7, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Schubert, Carsten	Exton	PA	US
Grasberger, Bruce	Trappe	PA	US
Maguire, Diane	Downington	PA	US
Deckman, Ingrid	Berwyn	PA	US
Spurlino, John	Downington	PA	US

US-CL-CURRENT: 435/226; 702/19

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 13. Document ID: US 20040132108 A1

L3: Entry 13 of 20 File: PGPB Jul 8, 2004

PGPUB-DOCUMENT-NUMBER: 20040132108
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040132108 A1

TITLE: Screening methods and agents

PUBLICATION-DATE: July 8, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Hupp, Theodore Robert	Dundee		GB
Dornan, David	Dundee		GB

US-CL-CURRENT: 435/7.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 14. Document ID: US 20040053262 A1

L3: Entry 14 of 20 File: PGPB Mar 18, 2004

PGPUB-DOCUMENT-NUMBER: 20040053262
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040053262 A1

TITLE: Supressor gene

PUBLICATION-DATE: March 18, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Lu, Xin	London		GB

US-CL-CURRENT: 435/6; 435/7.23

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 15. Document ID: US 20030194745 A1

L3: Entry 15 of 20 File: PGPB Oct 16, 2003

PGPUB-DOCUMENT-NUMBER: 20030194745
PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030194745 A1

TITLE: Cysteine mutants and methods for detecting ligand binding to biological molecules

PUBLICATION-DATE: October 16, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
McDowell, Robert S.	San Francisco	CA	US
Flanagan, W. Michael	Menlo Park	CA	US

US-CL-CURRENT: 435/7.1; 702/19

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 16. Document ID: US 20030149038 A1

L3: Entry 16 of 20 File: PGPB Aug 7, 2003

PGPUB-DOCUMENT-NUMBER: 20030149038
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030149038 A1

TITLE: Alpha-helix mimicry by a class of organic molecules

PUBLICATION-DATE: August 7, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Guy, Rodney K.	San Francisco	CA	US
Kuntz, Irwin D.	Greenbrae	CA	US
Lu, Felice	San Francisco	CA	US

US-CL-CURRENT: 514/234.5; 514/242, 514/248, 514/249, 514/252.02, 514/263.22, 514/307, 514/314, 514/332, 514/333, 544/112 , 544/115, 544/117, 544/236, 544/238, 544/277, 544/350, 544/353, 544/405, 546/148, 546/167, 546/256

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw D

☐ 17. Document ID: US 20030109518 A1

L3: Entry 17 of 20 File: PGPB Jun 12, 2003

PGPUB-DOCUMENT-NUMBER: 20030109518
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030109518 A1

TITLE: Substituted 1,4-benzodiazepines and uses thereof

PUBLICATION-DATE: June 12, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Lu, Tianbao	Kennett Square	PA	US
Lafrance, Louis V. III	West Chester	PA	US
Parks, Daniel J.	Exton	PA	US
Milkiewicz, Karen L.	Exton	PA	US
Calvo, Raul R.	Royersford	PA	US
Cummings, Maxwell D.	Wayne	PA	US
Kim, Alexander J.	Philadelphia	PA	US
Grasberger, Bruce L.	Trappe	PA	US
Carver, Theodore E. JR.	Downingtown	PA	US

US-CL-CURRENT: 514/221; 514/220, 540/495, 540/504, 540/505

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 18. Document ID: US 20020147173 A1

L3: Entry 18 of 20 File: PGPB Oct 10, 2002

PGPUB-DOCUMENT-NUMBER: 20020147173
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020147173 A1

TITLE: Methods of treatment using NBS-1, antibodies and proteins thereto, and uses of the antibodies

PUBLICATION-DATE: October 10, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Kaelin, William	Boston	MA	US
Jost, Christine	Jamaica Plain	MA	US

US-CL-CURRENT: 514/44; 435/7.23, 530/388.26, 530/388.8

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 19. Document ID: US 20020061539 A1

L3: Entry 19 of 20 File: PGPB May 23, 2002

PGPUB-DOCUMENT-NUMBER: 20020061539
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020061539 A1

TITLE: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR COACTIVATOR BINDING

PUBLICATION-DATE: May 23, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
BAXTER, JOHN D.	SAN FRANCISCO	CA	US
DARIMONT, BEATRICE	SAN FRANCISCO	CA	US
FENG, WEIJUN	SAN FRANCISCO	CA	US
FLETTERICK, ROBERT J.	SAN FRANCISCO	CA	US
KUSHNER, PETER J.	SAN FRANCISCO	CA	US
WAGNER, RICHARD L.	SAN FRANCISCO	CA	US
WEST, BRIAN L.	SAN FRANCISCO	CA	US
YAMAMOTO, KEITH R.	SAN FRANCISCO	CA	US

US-CL-CURRENT: 435/7.1; 257/E21.218, 257/E21.266, 435/183, 435/4, 702/19, 702/27

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 20. Document ID: US 20020051785 A1

L3: Entry 20 of 20 File: PGPB May 2, 2002

PGPUB-DOCUMENT-NUMBER: 20020051785
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020051785 A1

TITLE: HER -2/neu overexpression abrogates growth inhibitory pathways

PUBLICATION-DATE: May 2, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Slamon, Dennis J.	Woodland Hills	CA	US
Wilson, Cindy A.	Los Angeles	CA	US
Calzone, Frank J.	Westlake Village	CA	US

US-CL-CURRENT: 424/145.1; 514/44

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Terms	Documents
(human double minute 2 protein or hdm2 or mdm2) same crystal	20

Display Format: - Change Format

Hit List

First Hit Clear Generate Collection Print Fwd Refs Bkwd Refs
Generate OACS

Search Results - Record(s) 1 through 10 of 10 returned.

☐ 1. Document ID: US 20060099689 A1

```
L4: Entry 1 of 10                    File: PGPB                    May 11, 2006
```

PGPUB-DOCUMENT-NUMBER: 20060099689
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20060099689 A1

TITLE: Use of caspase enzymes for maturation of engineered recombinant polypeptide fusions

PUBLICATION-DATE: May 11, 2006

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Mertens; Nico M. A. C.	Melsele		BE
Kelly; Andrew Graham	Carcavelos		PT

US-CL-CURRENT: 435/69.7; 435/226, 435/252.33, 435/320.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 2. Document ID: US 20060063215 A1

```
L4: Entry 2 of 10                    File: PGPB                    Mar 23, 2006
```

PGPUB-DOCUMENT-NUMBER: 20060063215
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20060063215 A1

TITLE: Human GAK-related gene variants associated with lung cancer

PUBLICATION-DATE: March 23, 2006

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Dai; Ken-Shwo	Hsinchu		TW

US-CL-CURRENT: 435/7.23; 435/194, 435/320.1, 435/325, 435/69.1, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 3. Document ID: US 20060040285 A1

L4: Entry 3 of 10 File: PGPB Feb 23, 2006

PGPUB-DOCUMENT-NUMBER: 20060040285
PGPUB-FILING-TYPE:
DOCUMENT-IDENTIFIER: US 20060040285 A1

TITLE: Human kinase interacting protein 2 (KIP2)-related gene variant associated with cancers

PUBLICATION-DATE: February 23, 2006

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Dai; Ken-Shwo	Hsinchu		TW

US-CL-CURRENT: 435/6; 435/320.1, 435/325, 435/69.1, 435/7.23, 530/350, 530/388.8, 536/23.5 .

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 4. Document ID: US 20050037383 A1

L4: Entry 4 of 10 File: PGPB Feb 17, 2005

PGPUB-DOCUMENT-NUMBER: 20050037383
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20050037383 A1

TITLE: Soluble, stable form of HDM2, crystalline forms thereof and methods of use thereof

PUBLICATION-DATE: February 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Taremi, Shahriar Shane	Upper Montclair	NJ	US
Xie, Gaolian	Edison	NJ	US
Hesson, Thomas	Kendall Park	NJ	US
Duca, Jose S.	Cranford	NJ	US
Strickland, Corey	Martinsville	NJ	US
Windsor, William T.	East Brunswick	NJ	US
Madison, Vincent S.	Mountain Lakes	NJ	US
Zhang, Rumin	Edison	NJ	US
Reichert, Paul	Montville	NJ	US

US-CL-CURRENT: 435/6; 435/320.1, 435/325, 435/69.1, 530/350, 536/23.5

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 5. Document ID: US 20040265931 A1

L4: Entry 5 of 10 File: PGPB Dec 30, 2004

PGPUB-DOCUMENT-NUMBER: 20040265931
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040265931 A1

TITLE: HAUSP-Mdm2 interaction and uses thereof

PUBLICATION-DATE: December 30, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Gu, Wei	New York	NY	US
Li, Muyang	New York	NY	US

US-CL-CURRENT: 435/7.23

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 6. Document ID: US 20040197893 A1

L4: Entry 6 of 10 File: PGPB Oct 7, 2004

PGPUB-DOCUMENT-NUMBER: 20040197893
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040197893 A1

TITLE: HDM2-inhibitor complexes and uses thereof

PUBLICATION-DATE: October 7, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Schubert, Carsten	Exton	PA	US
Grasberger, Bruce	Trappe	PA	US
Maguire, Diane	Downington	PA	US
Deckman, Ingrid	Berwyn	PA	US
Spurlino, John	Downington	PA	US

US-CL-CURRENT: 435/226; 702/19

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 7. Document ID: US 20040161798 A1

L4: Entry 7 of 10 File: PGPB Aug 19, 2004

PGPUB-DOCUMENT-NUMBER: 20040161798
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040161798 A1

TITLE: Methods and compositions comprising capture agents

PUBLICATION-DATE: August 19, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Kodadek, Thomas	Dallas	TX	US

US-CL-CURRENT: 435/7.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 8. Document ID: US 20040053324 A1

L4: Entry 8 of 10 File: PGPB Mar 18, 2004

PGPUB-DOCUMENT-NUMBER: 20040053324
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20040053324 A1

TITLE: Assays and compositions for identifying agents that modulate the activity of deubiquitinating agents

PUBLICATION-DATE: March 18, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Wong, Brian	San Mateo	CA	US
Pray, Todd R.	San Francisco	CA	US
Huang, Jianing	Foster City	CA	US
Anderson, David	San Bruno	CA	US

US-CL-CURRENT: 435/7.1; 435/23

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 9. Document ID: US 20030108947 A1

L4: Entry 9 of 10 File: PGPB Jun 12, 2003

PGPUB-DOCUMENT-NUMBER: 20030108947
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030108947 A1

TITLE: Assays for identifying ubiquitin agents and for identifying agents that modify the activity of ubiquitin agents

PUBLICATION-DATE: June 12, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Issakani, Sarkiz D.	San Jose	CA	US
Huang, Jianing	Foster City	CA	US
Sheung, Julie	San Francisco	CA	US
Pray, Todd R.	San Francisco	CA	US

US-CL-CURRENT: 435/7.1; 435/23

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 10. Document ID: US 20030104474 A1

L4: Entry 10 of 10 File: PGPB Jun 5, 2003

PGPUB-DOCUMENT-NUMBER: 20030104474
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030104474 A1

TITLE: Assays for identifying ubiquitin agents and for identifying agents that modify the activity of ubiquitin agents

PUBLICATION-DATE: June 5, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY
Issakani, Sarkiz D.	San Jose	CA	US
Huang, Jianing	Foster City	CA	US
Sheung, Julie	San Francisco	CA	US
Pray, Todd R.	San Francisco	CA	US

US-CL-CURRENT: 435/7.1; 435/23

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Terms	Documents
(human double minute 2 protein or hdm2 or mdm2) same solid support	10

Display Format: CIT Change Format

Hit List

First Hit Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs
Generate OACS

Search Results - Record(s) 1 through 6 of 6 returned.

☐ 1. Document ID: US 7022510 B2
-: Invalid display element.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Des

---

☐ 2. Document ID: US 6979551 B2
-: Invalid display element.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Des

---

☐ 3. Document ID: US 6953669 B2
-: Invalid display element.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Des

---

☐ 4. Document ID: US 6919184 B2
-: Invalid display element.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Des

---

☐ 5. Document ID: US 6908755 B2
-: Invalid display element.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Des

---

☐ 6. Document ID: US 5702908 A

```
-:   Invalid display element.
```

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

---

Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs | Generate OACS

Terms	Documents
(human double minute 2 protein or hdm2 or mdm2) same solid support	6

Display Format: CIT | Change Format

Previous Page   Next Page   Go to Doc#